

Fig. 1 Binding of anti-IL13 mAbs to human IL-13 in ELISA

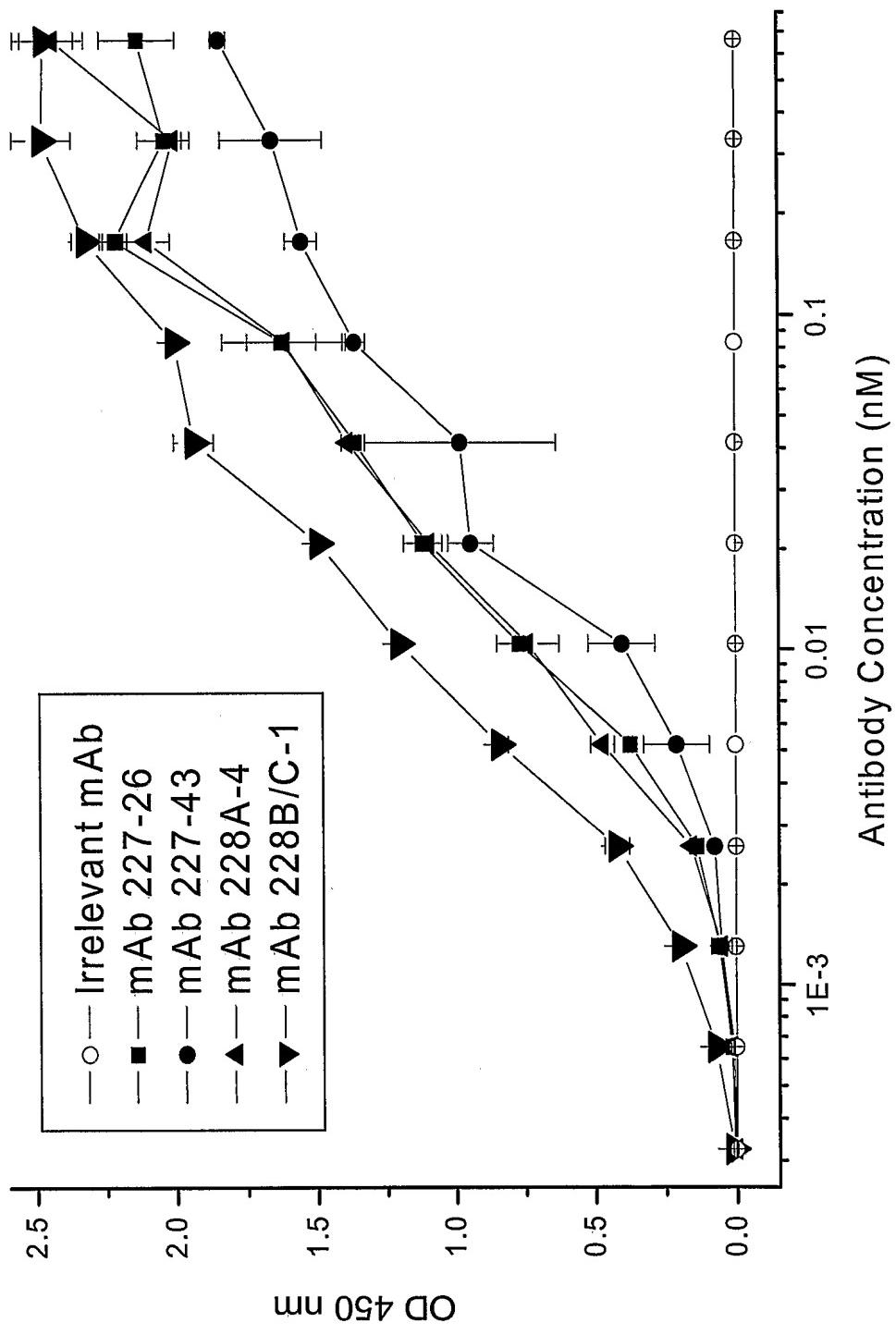


Fig. 2 Binding of anti-IL13 mAbs to MT-IL13/Fc

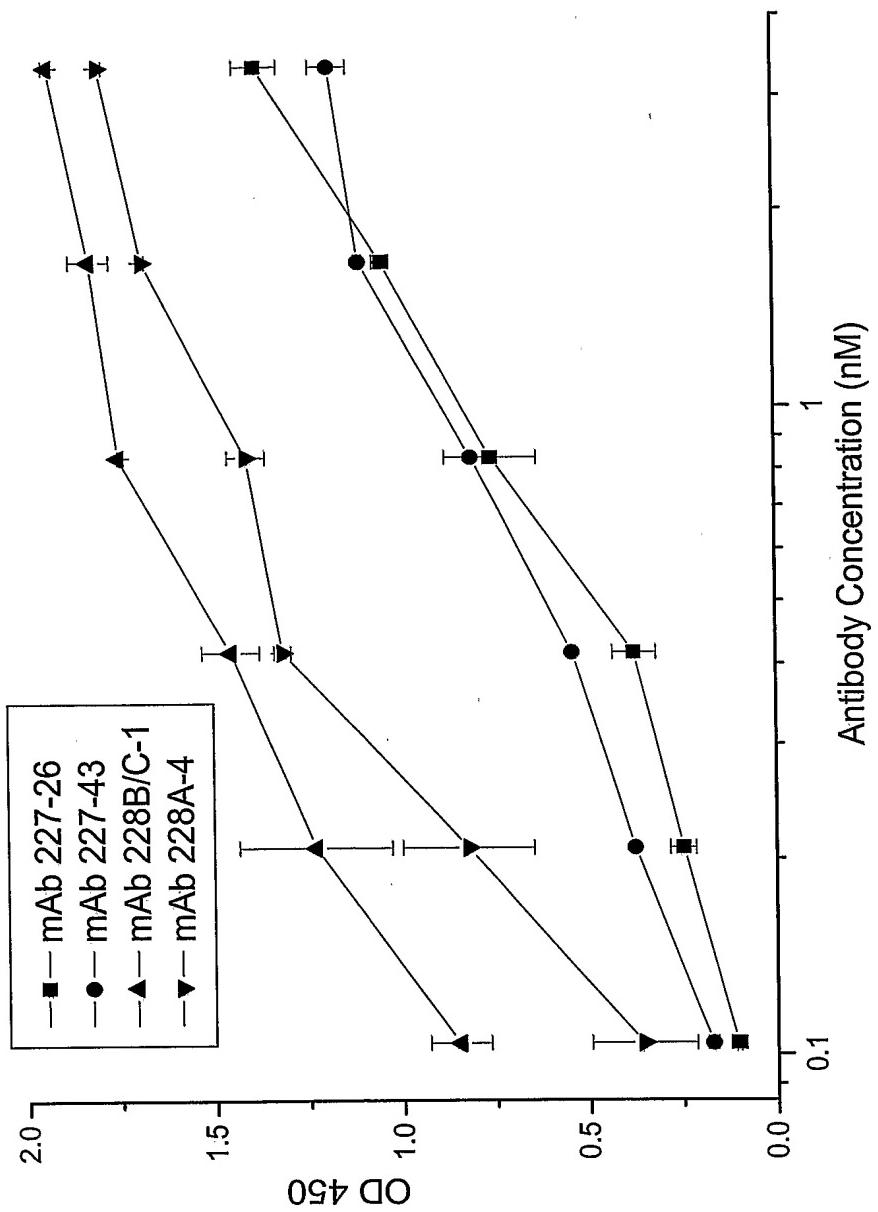


Fig. 3 Anti-IL13 mAb JES10-5A2 does not compete with the binding of mAb 228B/C-1-HRP to Human IL-13 in ELISA

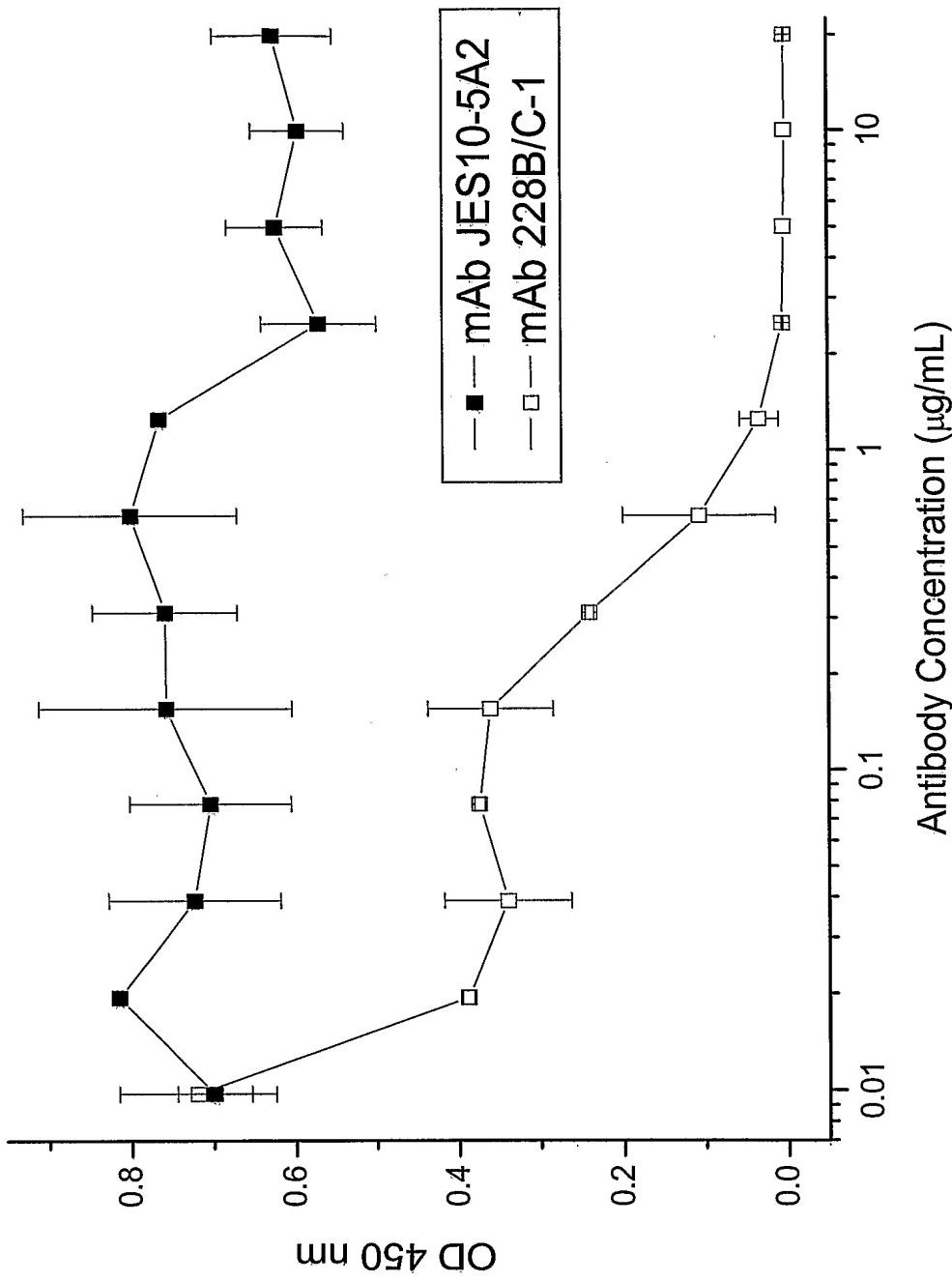


Fig. 4 Effect of anti-IL13 mAbs on the proliferation of L-1236 cells

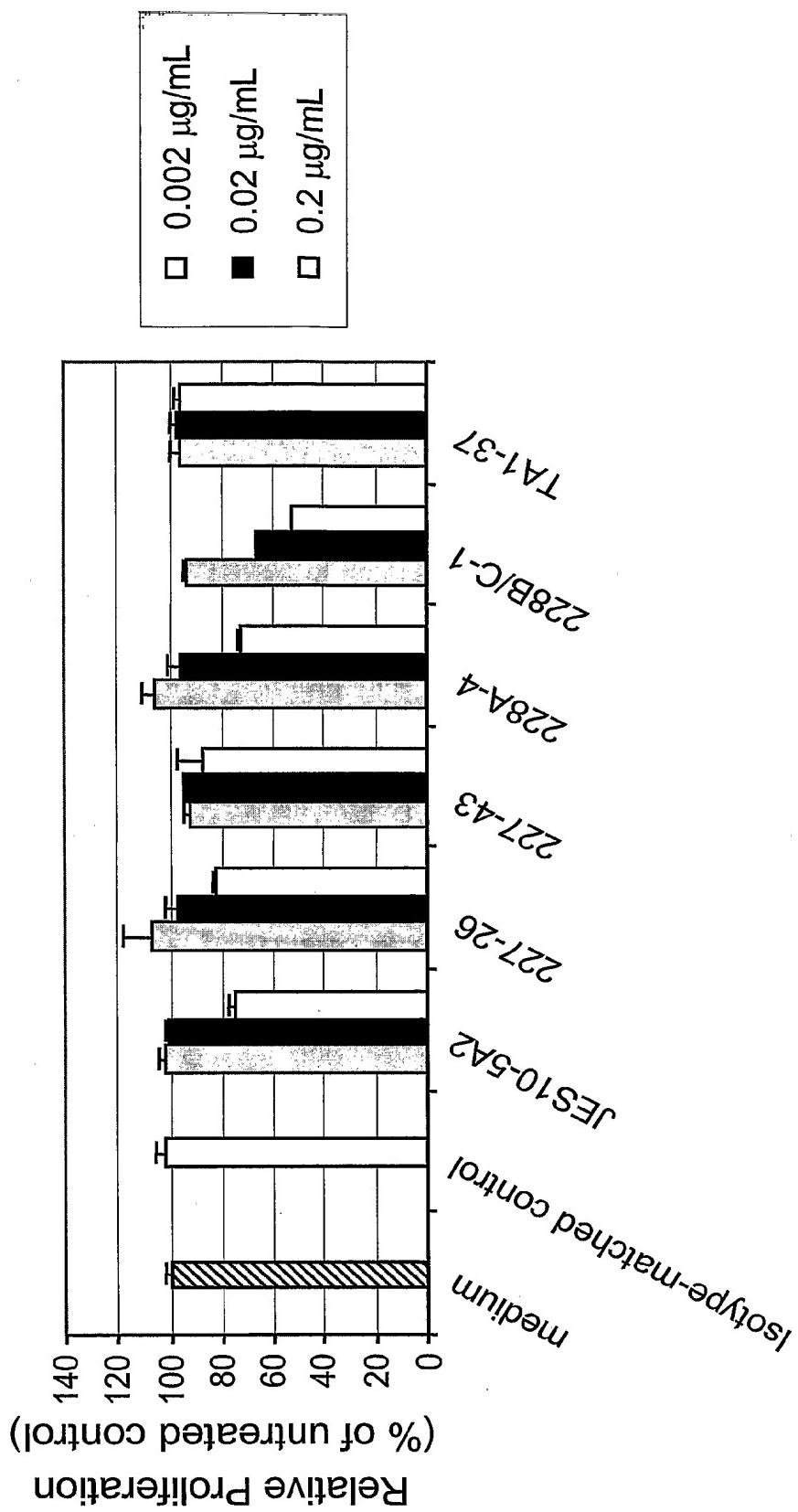


Fig. 5 Effect of anti-IL13 mAbs on IL13-induced suppression of CD14 expression in human monocytes

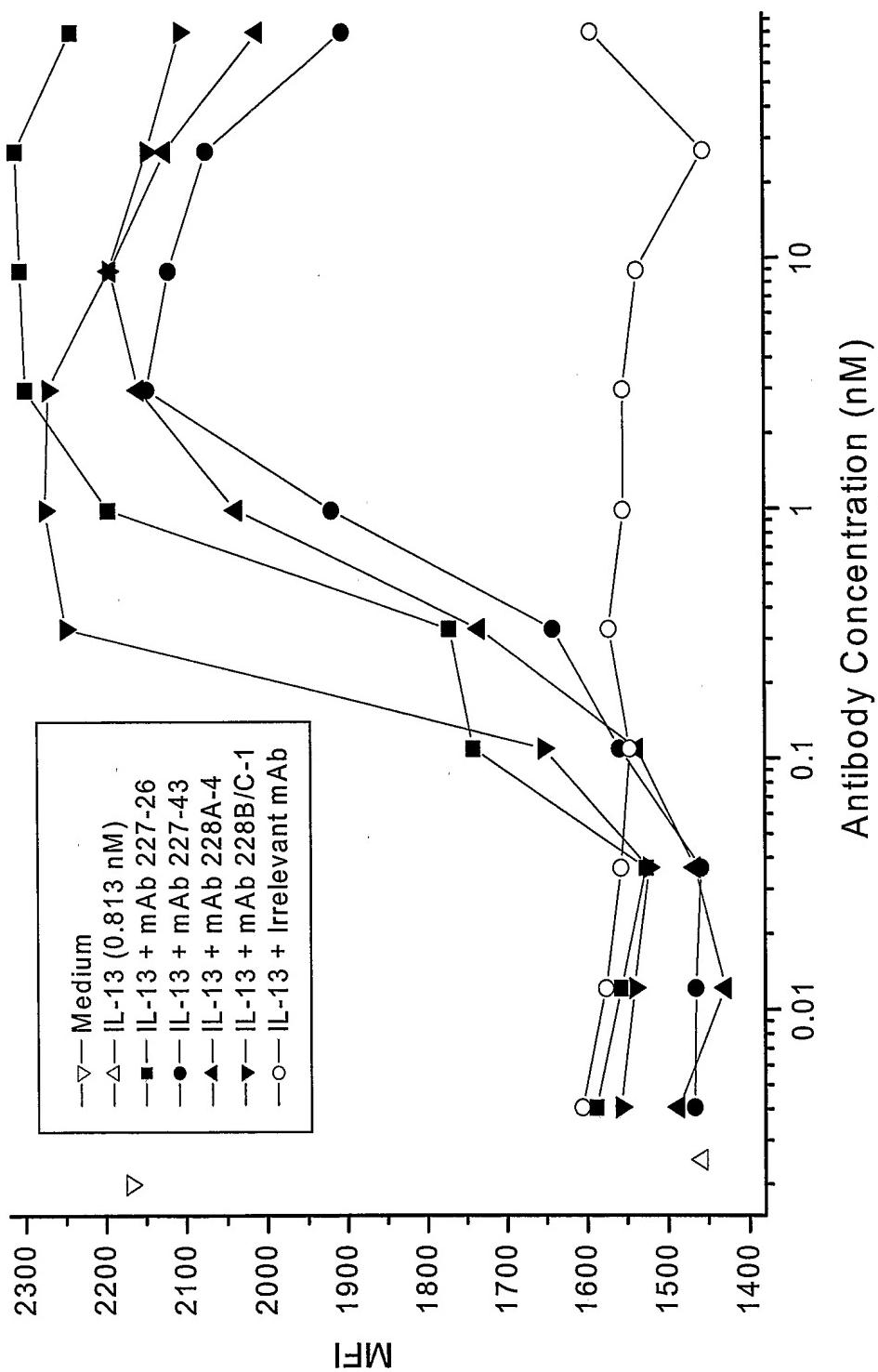


Fig. 6 Effect of anti-IL13 mAbs on IL13-induced upregulation of CD23 expression in human monocytes

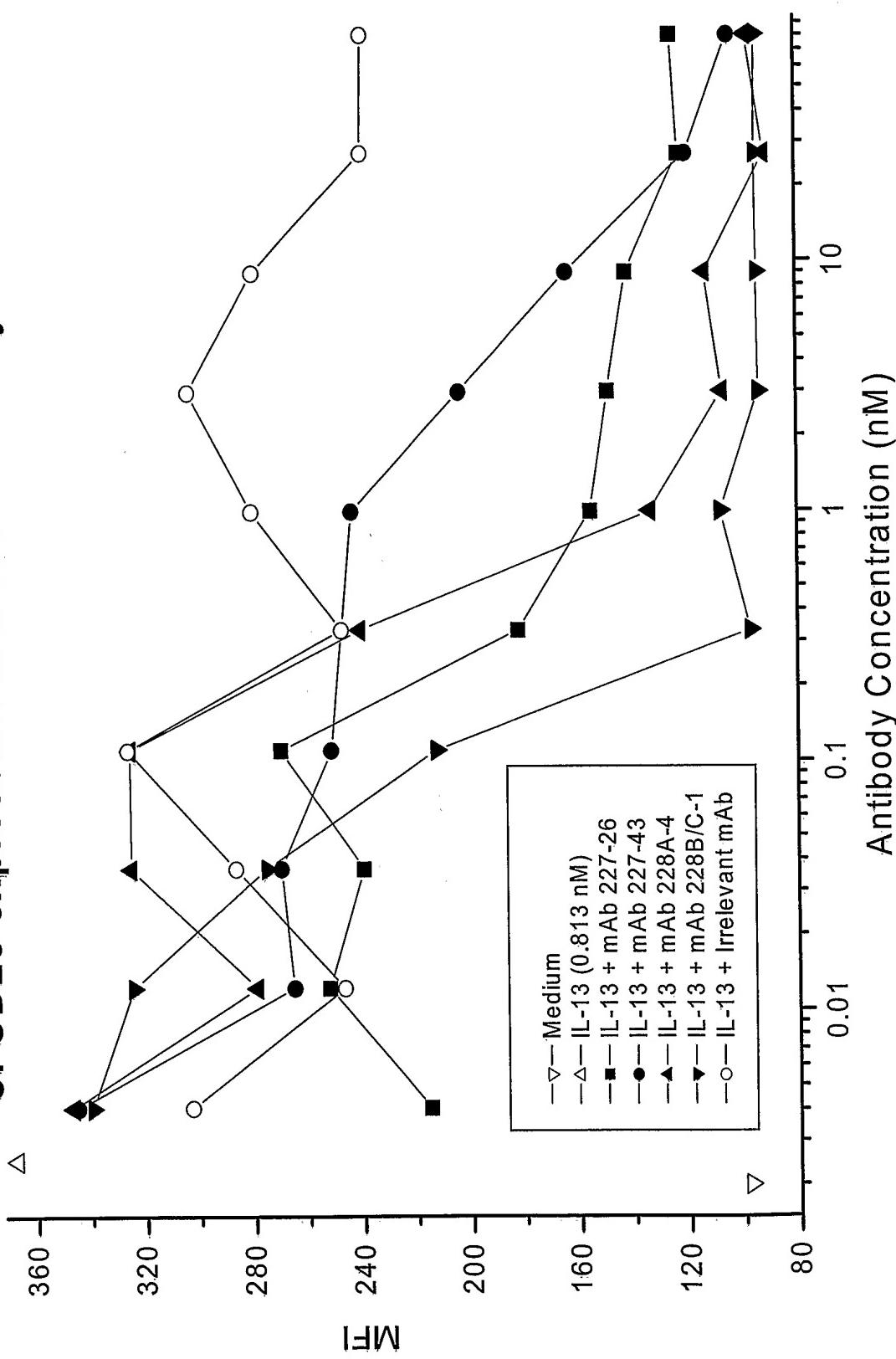


Fig. 7 Anti-IL13 mAbs Inhibit IL13-Induced Stat6 Phosphorylation in THP-1 Cells

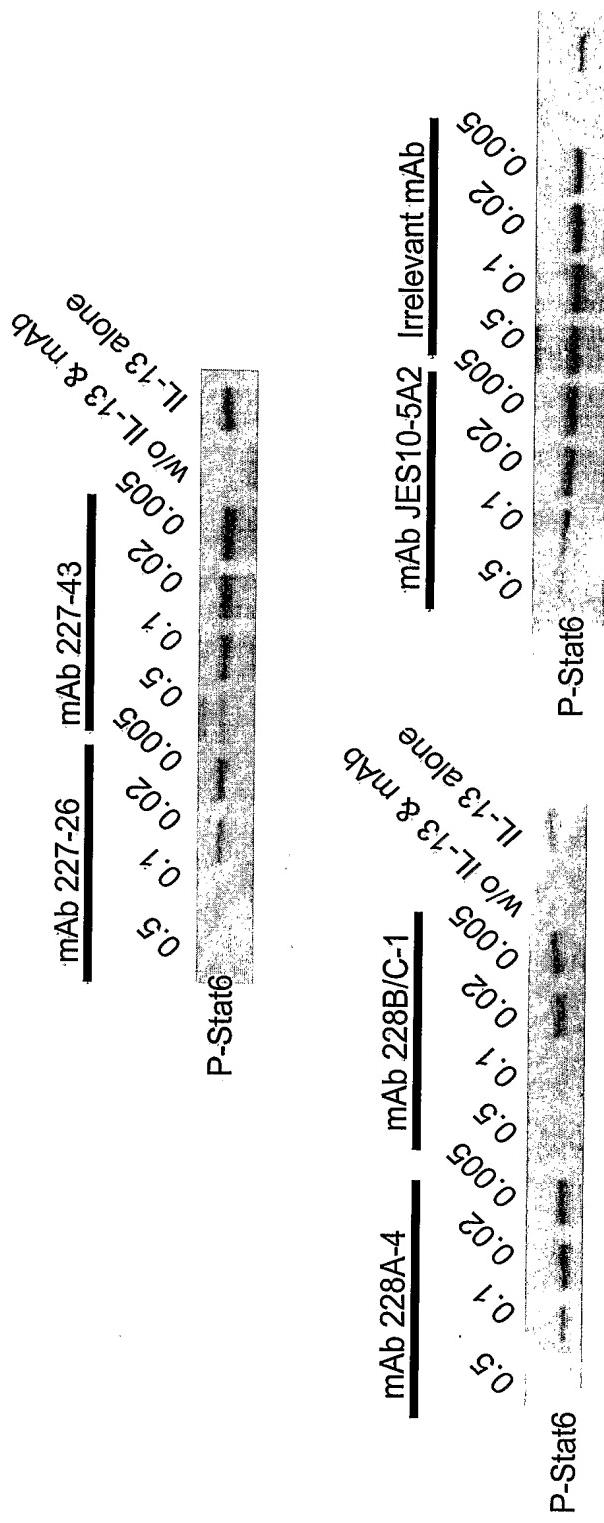


FIGURE 8**228B/C-1 Antibody**
Heavy Chain (VH)

1 Q V Q L Q E S G P G L V A P S Q S L S I T C T V S G F S L N A Y S V N W V	10 40 R Q P P G K G L E W L G M I W G D G K I V Y N S A L K S R L N I S K D S S	20 50 K S Q V F L K M S S L Q S D D T A R Y Y C A G D G Y Y P Y A M D N W G H G T	30 60 100 b c d e f 101
80 S V T V S S	82 90 118 (SEQ ID NO 4)	95 100	113 (SEQ ID NO 3)

Light Chain (VK)

10 N I V L T Q S P A S L A V S L G Q R A T I S C R A S K S V D S Y G N S F M H W	20 40 Y Q K P G Q P P K L L I Y L A S N L E S G V P A R F S G S G S R T D F T L T I	30 50 80 D P V E A D D A A S Y Y C Q Q N N E D P R T F G G G T K L E I K R A	70 100 113 (SEQ ID NO 3)

Underlined: Kabat CDR. Bold/Italic: Chothia CDR1.

FIGURE 9
228A-4 Antibody
Heavy Chain (VH)

<p>Light Chain (VK)</p> <pre> 1 N I V L T Q S P T S L A V S L G Q R A T I S C R A S E S V D S Y G N G F I H W 40 Y Q Q K P G Q P P K L I I Y I L A S N I E S G V P A R F S G S S R T D F T L T I 80 D P M E A D D A A T Y Y C Q Q N N E D P R T F G G G T K L E I K R A </pre>	<p>Heavy Chain (VH)</p> <pre> 1 Q V Q L I K E S G G P G I V A P S Q S L S I T C T V S G F S L T D Y N I N W I R Q 40 P P G K G L E W L G M I W G D G S T A Y N S A L K S R L S I S K D N S K S Q I F 80 82ab c 83 90 95 100 b c d e f 101 110 L K M N S L Q T E D T A R Y Y C A R D G Y F P Y A M A Y W G Q G T </pre>
118 S V T V S S	118 (SEQ ID NO 6)

Underlined: Kabat CDR. Bold/Italic: Chothia CDR1.

FIGURE 10
227-26 Antibody
Heavy Chain (VH)

Light Chain (VK)

1	10	20	30
	D V L M T Q T P L S L P V S L G D Q A S I S C R S S Q S I V H S S N G N T Y L Q		
40	50	60	70
	W Y L Q K P G Q S S P K L L I Y K V S N R F S G V P D R F S G S G S G T D F T L		
80	90	100	114
	I S R V E A E D L G V Y Y C F Q G S H V P Y T F G G T K L E I K R A		(S E)

Underlined: Kabat CDR. **Bold/Italic**: Chothia CDR1.

FIGURE 11 A

SEQ ID NO	VK CHAIN	FR1	FR2		CDR1	CDR2																			
			1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23
Murine 22B/C-1	N	I	V	L	T	Q	S	P	A	S	L	A	V	S	L	G	Q	R	A	T	I	S	C	20	W
Human female	D	I	V	M	T	Q	S	P	D	S	L	S	V	S	L	G	E	R	A	T	I	N	C	21	W
Clone B	D	I	V	M	T	Q	S	P	A	S	L	A	V	S	L	G	E	R	A	T	I	N	C	22	W
Clone J	D	I	V	L	T	Q	S	P	A	S	L	A	V	S	L	G	E	R	A	T	I	N	C	23	W
Clone L	D	I	V	L	T	Q	S	P	A	S	L	S	V	S	L	G	E	R	A	T	I	N	C	24	W
Clone N	D	I	V	L	T	Q	S	P	A	S	L	A	V	S	L	G	E	R	A	T	I	N	C	25	W
Clone P	D	I	V	L	T	Q	S	P	A	S	L	A	V	S	L	G	E	R	A	T	I	N	C	26	W
Clone R	D	I	V	L	T	Q	S	P	D	S	L	A	V	S	L	G	E	R	A	T	I	N	C	27	W
HT2-NEW #1	D	I	V	M	T	Q	S	P	D	S	L	S	V	S	L	G	E	R	A	T	I	N	C	28	W
HT2-NEW #9	D	I	V	M	T	Q	S	P	A	S	L	S	V	S	L	G	E	R	A	T	I	N	C	29	W
HT2-NEW #14	D	I	V	L	T	Q	S	P	D	S	L	S	V	S	L	G	E	R	A	T	I	N	C	30	W
HT2-NEW #17	D	I	V	L	T	Q	S	P	D	S	L	A	V	S	L	G	E	R	A	T	I	N	C	31	W
HT2-NEW #21	D	I	V	M	T	Q	S	P	D	S	L	S	V	S	L	G	E	R	A	T	I	N	C	32	W
HT2-NEW #26	D	I	V	L	T	Q	S	P	A	S	L	A	V	S	L	G	E	R	A	T	I	N	C	33	W
HT2-NEW #45	D	I	V	L	T	Q	S	P	D	S	L	A	V	S	L	G	E	R	A	T	I	N	C	34	W
HT2-NEW #57	D	I	V	L	T	Q	S	P	A	S	L	A	V	S	L	G	E	R	A	T	I	N	C	35	W
HT2-NEW #60	D	I	V	M	T	Q	S	P	D	S	L	S	V	S	L	G	E	R	A	T	I	N	C	36	W
HT2-NEW #73	D	I	V	L	T	Q	S	P	A	S	L	A	V	S	L	G	E	R	A	T	I	N	C	37	W
HT2-NEW #74	D	I	V	L	T	Q	S	P	D	S	L	A	V	S	L	G	E	R	A	T	I	N	C	38	W
HT2-NEW #78	D	I	V	L	T	Q	S	P	A	S	L	S	V	S	L	G	E	R	A	T	I	N	C	39	W
HT2-NEW #79	D	I	V	L	T	Q	S	P	A	S	L	A	V	S	L	G	E	R	A	T	I	N	C	40	W
HT2-NEW #80	D	I	V	M	T	Q	S	P	D	S	L	S	V	S	L	G	E	R	A	T	I	N	C	41	W
HT2-NEW #87	D	I	V	M	T	Q	S	P	D	S	L	A	V	S	L	G	E	R	A	T	I	N	C	42	W
HT2-NEW #75	D	I	V	L	T	Q	S	P	D	S	L	S	V	S	L	G	E	R	A	T	I	N	C	43	W
HT2-NEW #84	D	I	V	M	T	Q	S	P	A	S	L	A	V	S	L	G	E	R	A	T	I	N	C	44	W
HT2-NEW #91	D	I	V	L	T	Q	S	P	A	S	L	S	V	S	L	G	E	R	A	T	I	N	C	45	W
HT2-NEW #96	D	I	V	L	T	Q	S	P	D	S	L	S	V	S	L	G	E	R	A	T	I	N	C	46	W
HT2-NEW #102	D	I	V	M	T	Q	S	P	A	S	L	A	V	S	L	G	E	R	A	T	I	N	C	47	W
HT2-NEW #222	D	I	V	L	T	Q	S	P	D	S	L	A	V	S	L	G	E	R	A	T	I	N	C	48	W
HT2-NEW #111	D	I	V	L	T	Q	S	P	A	S	L	A	V	S	L	G	E	R	A	T	I	N	C	49	W
HT2-NEW #115	D	I	V	M	T	Q	S	P	D	S	L	S	V	S	L	G	E	R	A	T	I	N	C	50	W
HT2-NEW #116	D	I	V	L	T	Q	S	P	A	S	L	A	V	S	L	G	E	R	A	T	I	N	C	51	W
HT2-NEW #117	D	I	V	M	T	Q	S	P	D	S	L	S	V	S	L	G	E	R	A	T	I	N	C	52	W
HT2-NEW #143	D	I	V	L	T	Q	S	P	A	S	L	S	V	S	L	G	E	R	A	T	I	N	C	53	W
HT2-NEW #162	D	I	V	L	T	Q	S	P	D	S	L	S	V	S	L	G	E	R	A	T	I	N	C	54	W
HT2-NEW #139	D	I	V	M	T	Q	S	P	A	S	L	A	V	S	L	G	E	R	A	T	I	N	C	55	W
HT2-NEW #177	D	I	V	L	T	Q	S	P	D	S	L	S	V	S	L	G	E	R	A	T	I	N	C	56	W
HT2-NEW #313	D	I	V	L	T	Q	S	P	D	S	L	S	V	S	L	G	E	R	A	T	I	N	C	57	W

FIGURE 11C

FIGURE 11 B

SEQID	NO	FR4												FR5																																	
		63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	CDR3	463	104	105	106	107	108	109	110	111	112	113	114		
G	V	P	A	R	F	S	G	S	G	S	G	S	G	S	G	T	D	F	T	L	T	I	D	P	V	E	A	D	D	A	S	Y	Y	C	30	F	O	G	G	T	K	L	E	I	K	R	
G	V	P	D	R	F	S	G	S	G	S	G	S	G	S	G	T	D	F	T	L	T	I	D	P	L	Q	A	E	D	V	A	V	Y	Y	C	31	F	G	G	G	T	K	L	E	I	K	R
G	V	P	D	R	F	S	G	S	G	S	G	S	G	S	G	T	D	F	T	L	T	I	D	P	L	Q	A	E	D	V	A	V	Y	Y	C	32	F	G	G	G	T	K	L	E	I	K	R
G	V	P	D	R	F	S	G	S	G	S	G	S	G	S	G	T	D	F	T	L	T	I	D	P	V	Q	A	E	D	V	A	V	Y	Y	C	33	F	G	G	G	T	K	L	E	I	K	R
G	V	P	D	R	F	S	G	S	G	S	G	S	G	S	G	T	D	F	T	L	T	I	D	P	V	Q	A	E	D	V	A	V	Y	Y	C	34	F	G	G	G	T	K	L	E	I	K	R
G	V	P	D	R	F	S	G	S	G	S	G	S	G	S	G	T	D	F	T	L	T	I	D	P	V	Q	A	E	D	V	A	V	Y	Y	C	35	F	G	G	G	T	K	L	E	I	K	R
G	V	P	D	R	F	S	G	S	G	S	G	S	G	S	G	T	D	F	T	L	T	I	D	P	V	Q	A	E	D	V	A	V	Y	Y	C	36	F	G	G	G	T	K	L	E	I	K	R
G	V	P	D	R	F	S	G	S	G	S	G	S	G	S	G	T	D	F	T	L	T	I	D	P	V	Q	A	E	D	V	A	V	Y	Y	C	37	F	G	G	G	T	K	L	E	I	K	R
G	V	P	D	R	F	S	G	S	G	S	G	S	G	S	G	T	D	F	T	L	T	I	D	P	V	Q	A	E	D	V	A	V	Y	Y	C	38	F	G	G	G	T	K	V	E	I	K	R
G	V	P	D	R	F	S	G	S	G	S	G	S	G	S	G	T	D	F	T	L	T	I	D	P	V	Q	A	E	D	V	A	V	Y	Y	C	39	F	G	G	G	T	K	V	E	I	K	R
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G	V	P	D	R	F	S	G	S	G	S	G	S	G	S	G	T	D	F	T	L	T	I	D	P	V	Q	A	E	D	V	A	V	Y	Y	C	41	F	G	G	G	T	K	V	E	I	K	R
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G	V	P	D	R	F	S	G	S	G	S	G	S	G	S	G	T	D	F	T	L	T	I	D	P	V	Q	A	E	D	V	A	V	Y	Y	C	43	F	G	G	G	T	K	L	E	I	K	R
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G	V	P	D	R	F	S	G	S	G	S	G	S	G	S	G	T	D	F	T	L	T	I	D	P	V	Q	A	E	D	V	A	V	Y	Y	C	46	F	G	G	G	T	K	V	E	I	K	R
G	V	P	D	R	F	S	G	S	G	S	G	S	G	S	G	T	D	F	T	L	T	I	D	P	V	Q	A	E	D	V	A	V	Y	Y	C	47	F	G	G	G	T	K	L	E	I	K	R
G	V	P	D	R	F	S	G	S	G	S	G	S	G	S	G	T	D	F	T	L	T	I	D	P	V	Q	A	E	D	V	A	V	Y	Y	C	48	F	G	G	G	T	K	V	E	I	K	R
G	V	P	D	R	F	S	G	S	G	S	G	S	G	S	G	T	D	F	T	L	T	I	D	P	V	Q	A	E	D	V	A	V	Y	Y	C	49	F	G	G	G	T	K	V	E	I	K	R
G	V	P	D	R	F	S	G	S	G	S	G	S	G	S	G	T	D	F	T	L	T	I	D	P	V	Q	A	E	D	V	A	V	Y	Y	C	50	F	G	G	G	T	K	L	E	I	K	R
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G	V	P	D	R	F	S	G	S	G	S	G	S	G	S	G	T	D	F	T	L	T	I	D	P	V	Q	A	E	D	V	A	V	Y	Y	C	52	F	G	G	G	T	K	V	E	I	K	R
G	V	P	D	R	F	S	G	S	G	S	G	S	G	S	G	T	D	F	T	L	T	I	D	P	V	Q	A	E	D	V	A	V	Y	Y	C	53	F	G	G	G	T	K	V	E	I	K	R
G	V	P	D	R	F	S	G	S	G	S	G	S	G	S	G	T	D	F	T	L	T	I	D	P	V	Q	A	E	D	V	A	V	Y	Y	C	54	F	G	G	G	T	K	V	E	I	K	R
G	V	P	D	R	F	S	G	S	G	S	G	S	G	S	G	T	D	F	T	L	T	I	D	P	V	Q	A	E	D	V	A	V	Y	Y	C	55	F	G	G	G	T	K	V	E	I	K	R
G	V	P	D	R	F	S	G	S	G	S	G	S	G	S	G	T	D	F	T	L	T	I	D	P	V	Q	A	E	D	V	A	V	Y	Y	C	56	F	G	G	G	T	K	V	E	I	K	R

FIGURE 11 D

FIGURE 12A

FIGURE 12C

SEQ

FIGURE 12 B

FIGURE 12D

3

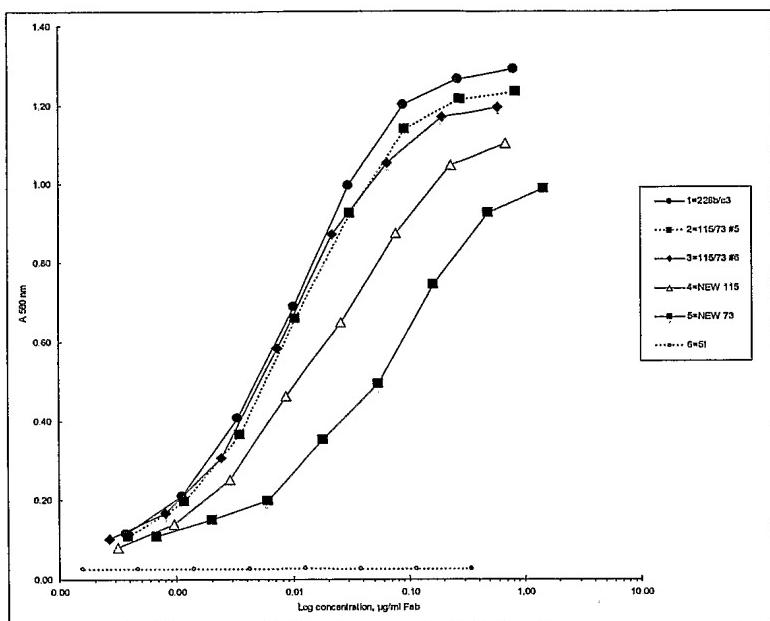
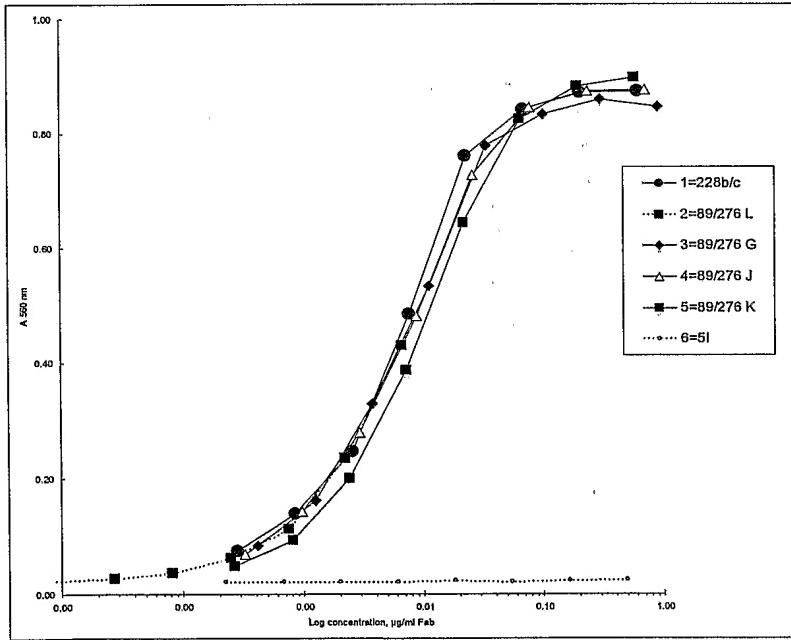
FIGURE 13 A**FIGURE 13 B**

FIGURE 13 C

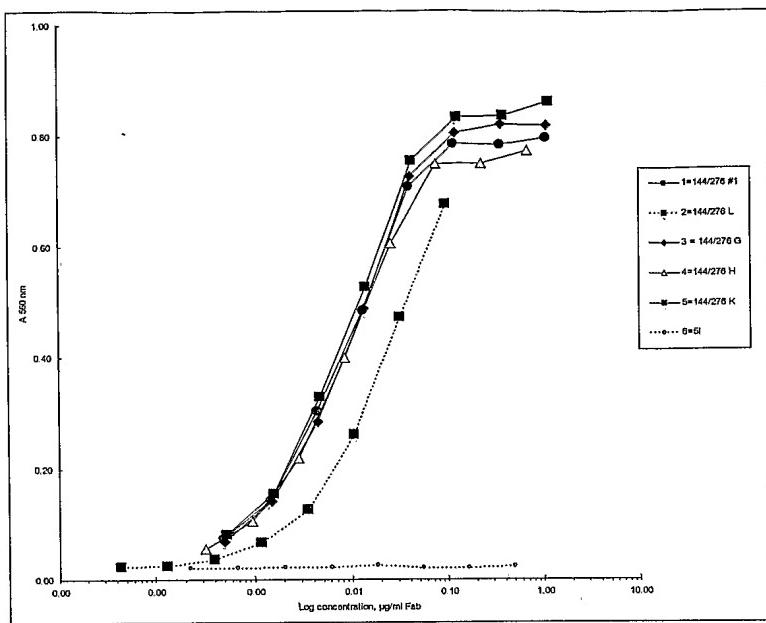


FIGURE 13 D

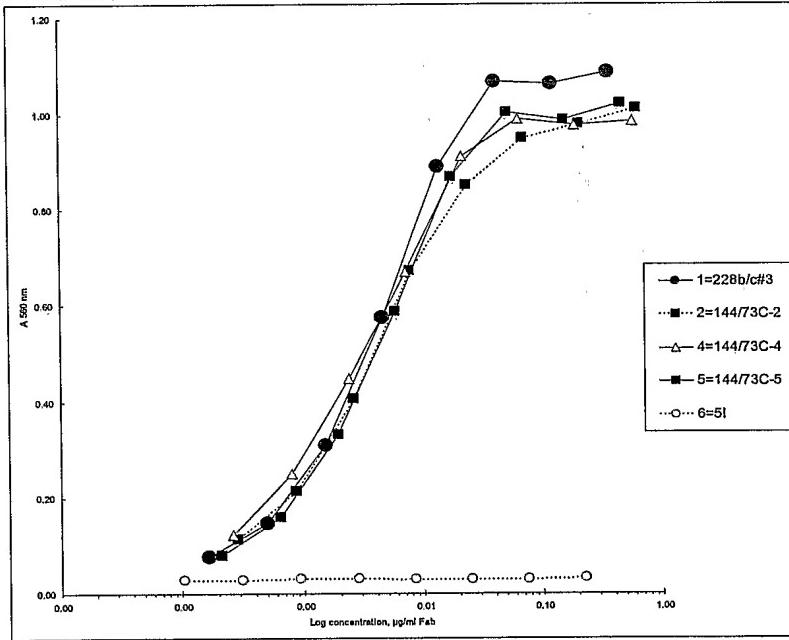


FIGURE 14 A

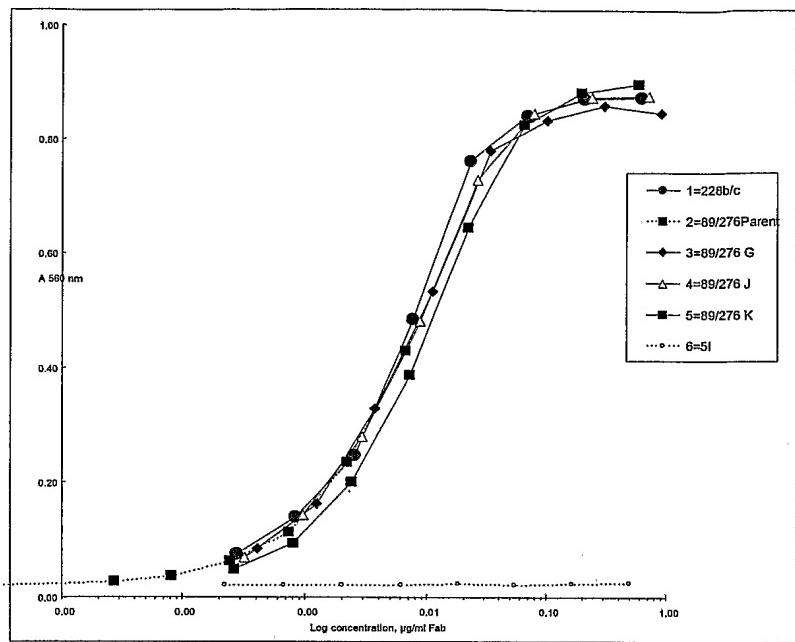


FIGURE 14B

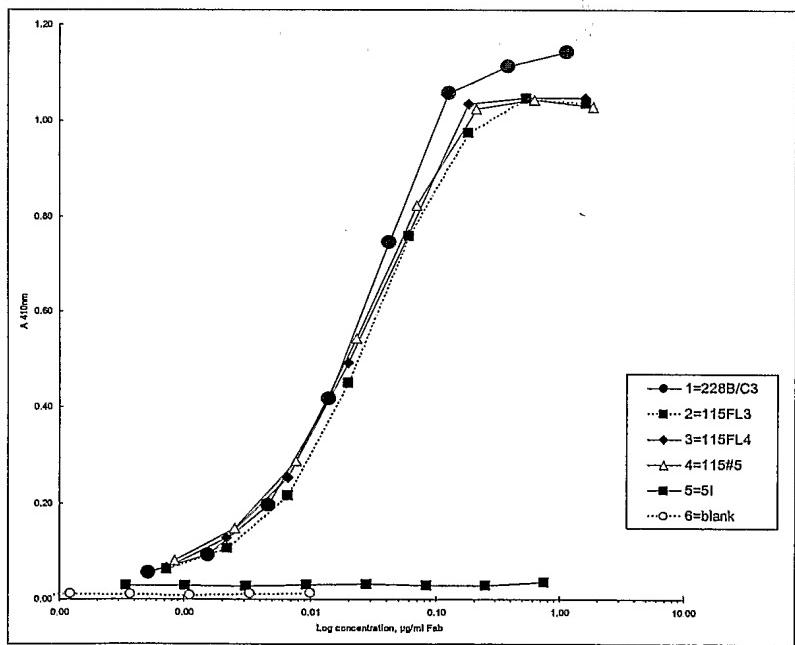


FIGURE 15

L1-59 (parent)	R	A	S	K	S	V	D	S	Y	G	Q	S	F	M	H
CDR-L1	R	A	S	K	S	V	D	S	Y	G	Q	S	F	M	H
CL-5	R	A	S	K	S	V	D	S	Y	G	Q	S	F	M	H
CL-13	R	A	S	K	S	V	D	S	Y	G	Q	S	F	M	H
CL-42	R	A	S	K	S	V	D	S	Y	G	Q	S	F	M	H
CL-48	R	A	S	K	S	V	D	S	Y	G	Q	S	F	M	H
CL-50	R	A	S	K	S	V	D	S	Y	G	Q	S	F	M	H
CL-56	R	A	S	K	S	V	D	S	Y	G	Q	S	F	M	H
CL-65	R	A	S	K	S	V	D	S	Y	G	Q	S	F	M	H
CL-69	R	A	S	K	S	V	D	S	Y	G	Q	S	F	M	H
CL-82	R	A	S	K	S	V	D	S	Y	G	Q	S	F	M	H
CL-94	R	A	S	K	S	V	D	S	Y	G	Q	S	F	M	H
L1-59 (parent)	Q	Q	N	N	E	D	P	R	T						
CDR-L3	Q	Q	N	N	E	D	P	R	T						
CL-5	Q	Q	N	A	E	D	P	R	T						
CL-13	Q	Q	N	N	E	D	P	R	T						
CL-42	Q	Q	N	A	E	D	P	R	T						
CL-48	Q	Q	N	N	E	D	P	R	T						
CL-50	Q	Q	N	A	E	D	P	R	T						
CL-56	Q	Q	N	A	E	D	P	R	T						
CL-65	Q	Q	N	N	E	D	P	R	T						
CL-69	Q	Q	N	A	E	D	P	R	T						
CL-82	Q	Q	N	N	E	D	P	R	T						
CL-94	Q	Q	N	A	E	D	P	R	T						
L1-59 (parent)	A	Y	S	V	N										
CDR-H1	A	Y	S	V	N										
CL-5	A	Y	S	V	N										
CL-13	A	K	S	V	N										
CL-42	A	N	S	V	N										
CL-48	A	N	S	V	N										
CL-50	A	K	S	V	N										
CL-56	A	K	S	V	N										
CL-65	A	S	S	V	N										
CL-69	A	N	S	V	N										
CL-82	A	N	S	V	N										
CL-94	A	N	S	V	N										
L1-59 (parent)	D	G	Y	Y	P	Y	A	M	D	N					
CDR-H3	D	G	Y	Y	P	Y	A	M	K	N					
CL-5	D	G	Y	Y	P	Y	A	M	K	N					
CL-13	D	G	Y	Y	P	Y	A	M	S	N					
CL-42	D	G	Y	Y	P	Y	A	M	K	N					
CL-48	D	G	Y	Y	P	Y	A	M	K	N					
CL-50	D	G	Y	Y	P	Y	A	M	K	N					
CL-56	D	G	Y	Y	P	Y	A	M	S	N					
CL-65	D	G	R	Y	P	Y	A	M	K	N					
CL-69	D	G	Y	Y	P	Y	A	M	D	N					
CL-82	D	G	Y	Y	P	Y	A	M	K	N					
CL-94	D	G	Y	Y	P	Y	A	M	K	N					

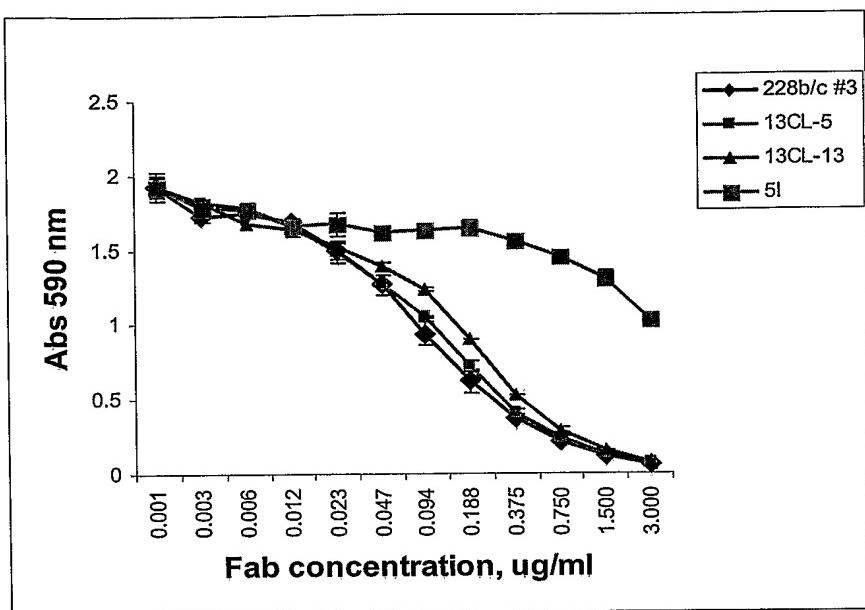
FIGURE 16

Figure 17 Variable Region Amino Acid Sequences for anti-II.13 Candidates

CL-5 (Affinity Matured Candidate) V_k:

DIVMTQSPDSLSSVSLGERATINCRASKSYDSYGGQSFMHWYQQKPGQPPKLLIYLASNLESGVPDRFSGSGSGTDFLT
 LTISLQAEDVAVYYCQQNAEDPRTFGGTTKVEIKR (SEQ ID NO 93)

CL-5 (Affinity Matured Candidate) V_h:

QVTLRESGPALVKPTQTLTCTGSFSSL~~SAYSVN~~WIRQPPGKALEWLAM~~MIWGDGKIVYNSALKSRLTISKDTSKN~~
 QVVLTMNTNMDPVVDATYYCAV~~DGYYPPYAMKNNWGGGS~~LVTVSS (SEQ ID NO 94)

CL-13 (Affinity Matured Candidate) V_k:

DIVMTQSPDSLSSVSLGERATINCRASKSYDSYGGQSFMHWYQQKPGQPPKLLIYLASNLESGVPDRFSGSGSGTDFLT
 LTISLQAEDVAVYYCQQNNEDPRTFGGTTKVEIKR (SEQ ID NO 95)

CL-13 (Affinity Matured Candidate) V_h:

QVTLRESGPALVKPTQTLTCTGSFSSL~~SAYSVN~~WIRQPPGKALEWLAM~~MIWGDGKIVYNSALKSRLTISKDTSKN~~
 QVVLTMNTNMDPVVDATYYCAV~~DGYYPPYAMKNNWGGGS~~LVTVSS (SEQ ID NO 96)

CL-50 (Affinity Matured Candidate) V_k:

DIVMTQSPDSLSSVSLGERATINCRASKSYDSYGGQSFMHWYQQKPGQPPKLLIYLASNLESGVPDRFSGSGSGTDFLT
 LTISLQAEDVAVYYCQQNAEDPRTFGGTTKVEIKR (SEQ ID NO 97)

CL-50 (Affinity Matured Candidate) V_h:

QVTLRESGPALVKPTQTLTCTGSFSSL~~SAYSVN~~WIRQPPGKALEWLAM~~MIWGDGKIVYNSALKSRLTISKDTSKN~~
 QVVLTMNTNMDPVVDATYYCAV~~DGYYPPYAMKNNWGGGS~~LVTVSS (SEQ ID NO 98)

FIGURE 18

Alignment of IL13 protein sequences

Figure 19 IL13 and the Binding Epitope of 228B/C MAb

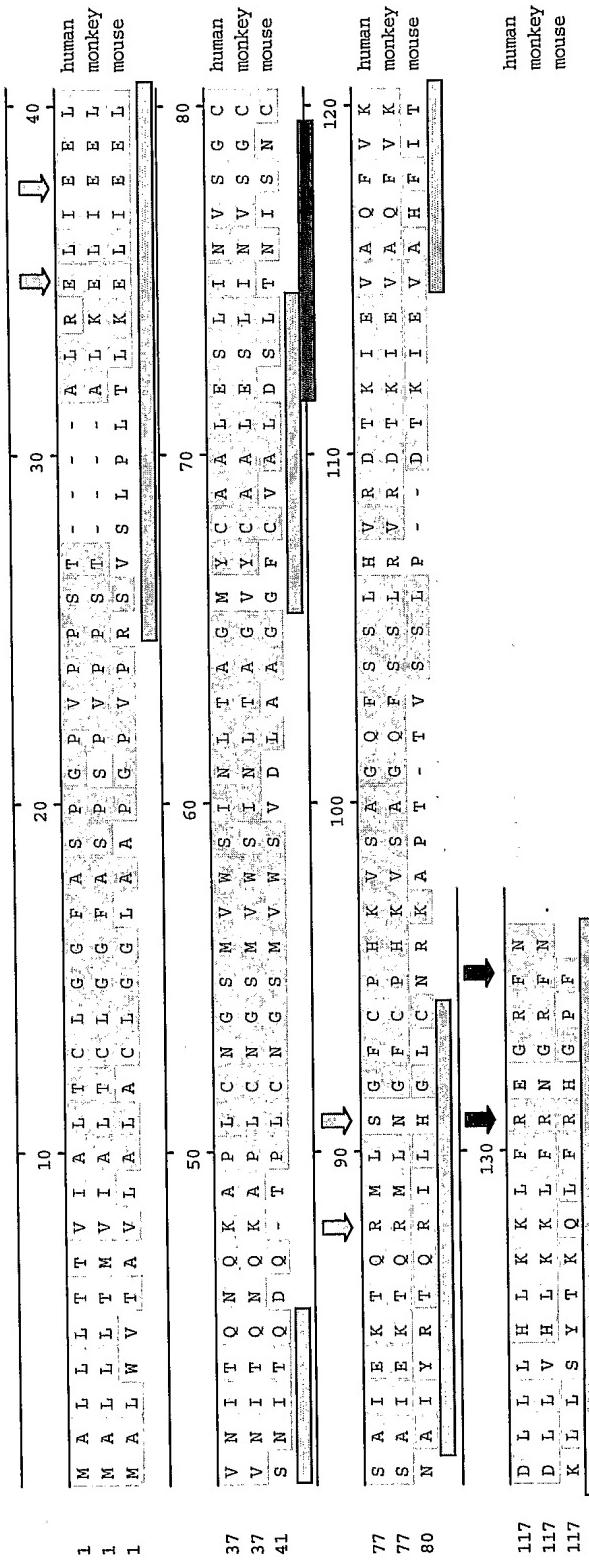


FIGURE 20

	CDR-L1			CDR-H1	
P	RASKSVDSYGNNSFMH	SEQ ID NO 99	P	AYSVN	SEQ ID NO 117
V1	RASKSVDSYGQSFMH	SEQ ID NO 100	V1	AKSVN	SEQ ID NO 118
V2	RASKSVDSYGQSFH	SEQ ID NO 101	V2	ANSVN	SEQ ID NO 119
V3	RASKSVDSYGNNSYMH	SEQ ID NO 102	V3	GYSVN	SEQ ID NO 120
V4	RASKSVDSYGNFLH	SEQ ID NO 103	V4	AHSVN	SEQ ID NO 121
			V5	ARSVN	SEQ ID NO 122
	CDR-L2			CDR-H2	
P	LASNLES	SEQ ID NO 104	P	MIWGDGKIVVNSALKS	SEQ ID NO 123
V1	LASNLLNS	SEQ ID NO 105	V1	MIWGDGKISVNSALKS	SEQ ID NO 124
V2	LASNLQS	SEQ ID NO 106	V2	MIWGDGKIVVNSALES	SEQ ID NO 125
V3	LATNLES	SEQ ID NO 107	V3	MIWGDGKIVVNSALKS	SEQ ID NO 126
V4	LASNLLKS	SEQ ID NO 108	V4	MIWGDGKIVVNSDLKS	SEQ ID NO 127
V5	LASNLEK	SEQ ID NO 109	V5	MIWGDGKVVVNSALKS	SEQ ID NO 128
V6	LASRLES	SEQ ID NO 110	V6	MIWGDGKIVVNSELKS	SEQ ID NO 129
V7	LASNLLHS	SEQ ID NO 111	V7	MIWGDGKIAVNSALKS	SEQ ID NO 130
V8	LASNLLSS	SEQ ID NO 112	V8	MIWGDGKIVVNSALKE	SEQ ID NO 131
V9	LASFLES	SEQ ID NO 113	V9	MVWDGKIVVNSALKS	SEQ ID NO 132
V10	LANNLES	SEQ ID NO 114	V10	MIWGDGKIVVNSALAS	SEQ ID NO 133
			V11	MIWGDGKKVNSALKS	SEQ ID NO 134
	CDR-L3			CDR-H3	
P	QQNNEDPRT	SEQ ID NO 115	P	DGYYPYAMDN	SEQ ID NO 135
V1	QQNAEDPRT	SEQ ID NO 116	V1	DGRYPYAMDN	SEQ ID NO 136
			V2	DGYYPYAMKN	SEQ ID NO 137
			V3	DGRYPYAMKN	SEQ ID NO 138
			V4	DGYYPYAMSN	SEQ ID NO 139
			V5	DGYYPYAMAN	SEQ ID NO 140
			V6	DGYYPYALDN	SEQ ID NO 141

FIGURE 21A: Variable Region Amino Acid Sequences for certain anti-IL13 Candidates:**CL-89 V_k (SEQ ID NO: 142):**

DIVMTQSPDSLSVSLGERATINCRASKSVDSYGNSFMHWWYQQKPPGQPPKLLIYLASNLESGVPDRFSSGGT
 DFTLTISLQAEDDVAVYCCQNNNEDPRTFGGGTKVEIKR

CL-276G V_h (SEQ ID NO 143):

QVTLRESGPALVKPTQTTLTCTVGFFSL SAYSVNWIRQPPGKALEWLAMIWGDGKIVYVNSALKSRLTISKDT
 KNQVVVLTMNTNMDPVDTATYYCAGDGYYPYAMDNWGGSLVTVSS

RL-36 (Random Library Candidate) V_k (SEQ ID NO 144):

DIVMTQSPDSLSVSLGERATINCRASKSVDSYGNSFMHWWYQQKPPGQPPKLLIYLASNLESGVPDRFSSGGT
 DFTLTISLQAEDDVAVYCCQNNNEDPRTFGGGTKVEIKR

RL-36 (Random Library Candidate) V_h (SEQ ID NO 145):

QVTLRESGPALVKPTQTTLTCTGSFFSL SAYSVNWIRQPPGKALEWLAMIWGDGKIVYVNSALKSRLTISKDT
 KNQVVVLTMNTNMDPVDTATYYCAVDGYYPYAMDNWGGSLVTV
 SS

RL-19 (Random Library Candidate) V_h (SEQ ID NO 146):

QVTLRESGPALVKPTQTTLTCTSSGFSL SAYSVNWIRQPPGKALEWLAMIWGDGKIVYVNSALKSRLTISKDT
 KNQVVVLTMNTNMDPVDTATYYCALDGYYPYAMDNWGGSLVTV
 SS

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FIGURE 21B: Variable Region Amino Acid Sequences for certain anti-IL13 Candidates:
RL-11 (Random Library Candidate) Vh (SEQ ID NO 147);

RL-11 (Random Library Candidate) Vh (SEQ ID NO 147):

QVTLRESGPALVKPTQTLTCTTSFGFLSAYSVNWIRQPPGKALEWLAMIWGDGKIVYNSALKSRLTISKDTS
KNQVVLTMTNMDPVDTATYYCAVDGYYPYAMDNWGQGSLOTV
SS

RL-8 (Random Library Candidate) Vh (SEQ ID NO 148):

QVTLRESGPALVKPTQTLLTCTLSGFSLSAYSVN
WIRQPPGKALEWLAMIWGDGKIVYNSALKSR
LTISKDTSK
NQVVLTMTNMDPVDTATYYCASDGYYPYAMDNWGGSLVTV
SS

RL-45 (Random Library Candidate) Vh(SEQ ID NO 149);

QVTLRESGPALVKPTQT
TCTSGFSLAYSVNWIRQPPGKALEWLAM
KNQVVLMTNMDPVDTATYYCATDGYYPYAMDNW
SS

RL36-L1.59 (L1 Affinity Matured Candidate) V_k (SEQ ID NO 150):

DIVMTQSPDSSLVSVLGERATINCRAKSVDSYQQSFMHWYQQKPGQPPPKLILYLASNLESGVPDRFSGSGSGT
DFTLTSSQLQAEDVAVYCCQNNEDPRTFGGGTKVEIKR

RL36-L1,59 (L1 Affinity Matured Candidate) Vh (SEQ ID NO 151):
QVTLLRESGPALVKPTQTLLTCTGSGFSLSAYSVNWIRQPPGKALEWLAMIWGDGKIVYNSALKSRLTISKDTS
KNQVVVLTMNMDPVDTATYYCAVDGYYPYAMDNWGQQGLVTSS

scFV Candidate #212 (SEQ ID NO 152):

QVTLRESGPALVKPTQTLLTCTVSGFSLSSAYSVNWIRQPPGKALEWLAMIWGDGKIVYNSALKSRLTISKDTS
KNQVVVLTMNTNMDPVDTATYYCAGDGYYPYAMDNWGGQGSVLTV
SSGGSSRSSSSGGGGGGGGDIVMTQSPDSLSSVSLGERATINGCRASSSVDSYGNNSFMHWYQQKPGQPPPCKLLI
YLASNLESGVPDRFSGSGSGTDFTLTISVQAEDVAVYCCQN
NEDPRTFGGGTKVEIKR